RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/519,083_

Source: _PCT/10_

Date Processed by STIC: _1/10/05_

ENTERED

RAW SEQUENCE LISTING   DATE: 01/10/2005
PATENT APPLICATION: US/10/519,083   TIME: 15:45:00

Input Set : A:\004974.01057 sequence listing.txt.TXT
Output Set: N:\CRF4\01102005\J519083.raw

```
 4 <110> APPLICANT: Bayer AG
 5         Bayerwerk
 6         51368 Leverkusen
 8 <120> TITLE OF INVENTION: Regulation of Human Receptor Tyrosine Kinase MerTK
10 <130> FILE REFERENCE: Lio496 WO
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/519,083
C--> 12 <141> CURRENT FILING DATE: 2004-12-23
12 <150> PRIOR APPLICATION NUMBER: US 60/391,933
13 <151> PRIOR FILING DATE: 2002-06-28
15 <150> PRIOR APPLICATION NUMBER: US 60/432,669
16 <151> PRIOR FILING DATE: 2002-12-12
18 <160> NUMBER OF SEQ ID NOS: 21
20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 3248
24 <212> TYPE: DNA
25 <213> ORGANISM: Homo sapiens
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (101)...(3151)
31 <400> SEQUENCE: 1
32 acagggagct tcgctggcgc gcttggccgg cgacaggaca ggttcgggac gtccatctgt 60
33 ccatccgtcc ggagagaaat tacagatccg cagccccggg atg ggg ccg gcc ccg   115
34                                                Met Gly Pro Ala Pro
35                                                 1               5.
37 ctg ccg ctg ctg ctg ggc ctc ttc ctc ccc gcg ctc tgg cgt aga gct   163
38 Leu Pro Leu Leu Leu Gly Leu Phe Leu Pro Ala Leu Trp Arg Arg Ala
39                 10                  15                  20
41 atc act gag gca agg gaa gaa gcc aag cct tac ccg cta ttc ccg gga   211
42 Ile Thr Glu Ala Arg Glu Glu Ala Lys Pro Tyr Pro Leu Phe Pro Gly
43             25                  30                  35
45 cct ttt cca ggg agc ctg caa act gac cac aca ccg ctg tta tcc ctt   259
46 Pro Phe Pro Gly Ser Leu Gln Thr Asp His Thr Pro Leu Leu Ser Leu
47             40                  45                  50
49 cct cac gcc agt ggg tac cag cct gcc ttg atg ttt tca cca acc cag   307
50 Pro His Ala Ser Gly Tyr Gln Pro Ala Leu Met Phe Ser Pro Thr Gln
51     55                  60                  65
53 cct gga aga cca cat aca gga aac gta gcc att ccc cag gtg acc tct   355
54 Pro Gly Arg Pro His Thr Gly Asn Val Ala Ile Pro Gln Val Thr Ser
55 70                  75                  80                  85
57 gtc gaa tca aag ccc cta ccg cct ctt gcc ttc aaa cac aca gtt gga   403
58 Val Glu Ser Lys Pro Leu Pro Pro Leu Ala Phe Lys His Thr Val Gly
59                 90                  95                 100
```

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```
61 cac ata ata ctt tct gaa cat aaa ggt gtc aaa ttt aat tgc tca atc   451
62 His Ile Ile Leu Ser Glu His Lys Gly Val Lys Phe Asn Cys Ser Ile
63             105             110             115
65 agt gta cct aat ata tac cag gac acc aca att tct tgg tgg aaa gat   499
66 Ser Val Pro Asn Ile Tyr Gln Asp Thr Thr Ile Ser Trp Trp Lys Asp
67             120             125             130
69 ggg aag gaa ttg ctt ggg gca cat cat gca att aca cag ttt tat cca   547
70 Gly Lys Glu Leu Leu Gly Ala His His Ala Ile Thr Gln Phe Tyr Pro
71     135             140             145
73 gat gat gaa gtt aca gca ata atc gct tcc ttc agc ata acc agt gtg   595
74 Asp Asp Glu Val Thr Ala Ile Ile Ala Ser Phe Ser Ile Thr Ser Val
75 150             155             160             165
77 cag cgt tca gac aat ggg tcg tat atc tgt aag atg aaa ata aac aat   643
78 Gln Arg Ser Asp Asn Gly Ser Tyr Ile Cys Lys Met Lys Ile Asn Asn
79             170             175             180
81 gaa gag atc gtg tct gat ccc atc tac atc gaa gta caa gga ctt cct   691
82 Glu Glu Ile Val Ser Asp Pro Ile Tyr Ile Glu Val Gln Gly Leu Pro
83             185             190             195
85 cac ttt act aag cag cct gag agc atg aat gtc acc aga aac aca gcc   739
86 His Phe Thr Lys Gln Pro Glu Ser Met Asn Val Thr Arg Asn Thr Ala
87     200             205             210
89 ttc aac ctc acc tgt cag gct gtg ggc ccg cct gag ccc gtc aac att   787
90 Phe Asn Leu Thr Cys Gln Ala Val Gly Pro Pro Glu Pro Val Asn Ile
91     215             220             225
93 ttc tgg gtt caa aac agt agc cgt gtt aac gaa cag cct gaa aaa tcc   835
94 Phe Trp Val Gln Asn Ser Ser Arg Val Asn Glu Gln Pro Glu Lys Ser
95 230             235             240             245
97 ccc tcc gtg cta act gtt cca ggc ctg acg gag atg gcg gtc ttc agt   883
98 Pro Ser Val Leu Thr Val Pro Gly Leu Thr Glu Met Ala Val Phe Ser
99             250             255             260
101 tgt gag gcc cac aat gac aaa ggg ctg acc gtg tcc aag gga gtg cag   931
102 Cys Glu Ala His Asn Asp Lys Gly Leu Thr Val Ser Lys Gly Val Gln
103             265             270             275
105 atc aac atc aaa gca att ccc tcc cca cca act gaa gtc agc atc cgt   979
106 Ile Asn Ile Lys Ala Ile Pro Ser Pro Pro Thr Glu Val Ser Ile Arg
107             280             285             290
109 aac agc act gca cac agc att ctg atc tcc tgg gtt cct ggt ttt gat  1027
110 Asn Ser Thr Ala His Ser Ile Leu Ile Ser Trp Val Pro Gly Phe Asp
111     295             300             305
113 gga tac tcc ccg ttc agg aat tgc agc att cag gtc aag gaa gct gat  1075
114 Gly Tyr Ser Pro Phe Arg Asn Cys Ser Ile Gln Val Lys Glu Ala Asp
115 310             315             320             325
117 ccg ctg agt aat ggc tca gtc atg att ttt aac acc tct gcc tta cca  1123
118 Pro Leu Ser Asn Gly Ser Val Met Ile Phe Asn Thr Ser Ala Leu Pro
119             330             335             340
121 cat ctg tac caa atc aag cag ctg caa gcc ctg gct aat tac agc att  1171
122 His Leu Tyr Gln Ile Lys Gln Leu Gln Ala Leu Ala Asn Tyr Ser Ile
123             345             350             355
125 ggt gtt tcc tgc atg aat gaa ata ggc tgg tct gca gtg agc cct tgg  1219
```

```
126 Gly Val Ser Cys Met Asn Glu Ile Gly Trp Ser Ala Val Ser Pro Trp
127         360   —             365             370       ..   —
129 att cta gcc agc acg act gaa gga gcc cca tca gta gca cct tta aat   1267
130 Ile Leu Ala Ser Thr Thr Glu Gly Ala Pro Ser Val Ala Pro Leu Asn
131         375             380             385
133 gtc act gtg ttt ctg aat gaa tct agt gat aat gtg gac atc aga tgg   1315
134 Val Thr Val Phe Leu Asn Glu Ser Ser Asp Asn Val Asp Ile Arg Trp
135 390             395             400             405         .
137 atg aag cct ccg act aag cag cag gat gga gaa ctg gtg ggc tac cgg   1363
138 Met Lys Pro Pro Thr Lys Gln Gln Asp Gly Glu Leu Val Gly Tyr Arg
139         410             415             420
141 ata tcc cac gtg tgg cag agt gca ggg att tcc aaa gag ctc ttg gag   1411
142 Ile Ser His Val Trp Gln Ser Ala Gly Ile Ser Lys Glu Leu Leu Glu
143         425             430             435
145 gaa gtt ggc cag aat ggc agc cga gct cgg atc tct gtt caa gtc cac   1459
146 Glu Val Gly Gln Asn Gly Ser Arg Ala Arg Ile Ser Val Gln Val His
147         440             445             450
149 aat gct acg tgc aca gtg agg att gca gcc gtc acc aga ggg gga gtt   1507
150 Asn Ala Thr Cys Thr Val Arg Ile Ala Ala Val Thr Arg Gly Gly Val
151         455             460             465
153 ggg ccc ttc agt gat cca gtg aaa ata ttt atc cct gca cac ggt tgg   1555
154 Gly Pro Phe Ser Asp Pro Val Lys Ile Phe Ile Pro Ala His Gly Trp
155 470             475             480             485
157 gta gat tat gcc ccc tct tca act ccg gcg cct ggc aac gca gat cct   1603
158 Val Asp Tyr Ala Pro Ser Ser Thr Pro Ala Pro Gly Asn Ala Asp Pro
159         490             495             500
161 gtg ctc atc atc ttt ggc tgc ttt tgt gga ttt att ttg att ggg ttg   1651
162 Val Leu Ile Ile Phe Gly Cys Phe Cys Gly Phe Ile Leu Ile Gly Leu
163         505             510             515
165 att tta tac atc tcc ttg gcc atc aga aaa aga gtc cag gag aca aag   1699
166 Ile Leu Tyr Ile Ser Leu Ala Ile Arg Lys Arg Val Gln Glu Thr Lys
167         520             525             530
169 ttt ggg aat gca ttc aca gag gag gat tct gaa tta gtg gtg aat tat   1747
170 Phe Gly Asn Ala Phe Thr Glu Glu Asp Ser Glu Leu Val Val Asn Tyr
171 535             540             545
173 ata gca aag aaa tcc ttc tgt cgg cga gcc att gaa ctt acc tta cat   1795
174 Ile Ala Lys Lys Ser Phe Cys Arg Arg Ala Ile Glu Leu Thr Leu His
175 550             555             560             565
177 agc ttg gga gtc agt gag gaa cta caa aat aaa cta gaa gat gtt gtg   1843
178 Ser Leu Gly Val Ser Glu Glu Leu Gln Asn Lys Leu Glu Asp Val Val
179         570             575             580
181 att gac agg aat ctt cta att ctt gga aaa att ctg ggt gaa gga gag   1891
182 Ile Asp Arg Asn Leu Leu Ile Leu Gly Lys Ile Leu Gly Glu Gly Glu
183         585             590           · 595
185 ttt ggg tct gta atg gaa gga aat ctt aag cag gaa gat ggg acc tct   1939
186 Phe Gly Ser Val Met Glu Gly Asn Leu Lys Gln Glu Asp Gly Thr Ser
187         600             605             610
189 ctg aaa gtg gca gtg aag acc atg aag ttg gac aac tct tca cag cgg   1987
190 Leu Lys Val Ala Val Lys Thr Met Lys Leu Asp Asn Ser Ser Gln Arg
```

RAW SEQUENCE LISTING   DATE: 01/10/2005
PATENT APPLICATION: US/10/519,083   TIME: 15:45:00

Input Set : A:\004974.01057 sequence listing.txt.TXT
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```
191    615                    620                  625
193 gag atc gag gag ttt ctc agt gag gca gcg tgc atg aaa gac ttc agc   2035
194 Glu Ile Glu Glu Phe Leu Ser Glu Ala Ala Cys Met Lys Asp Phe Ser
195 630                    635                  640                  645
197 cac cca aat gtc att cga ctt cta ggt gtg tgt ata gaa atg agc tct   2083
198 His Pro Asn Val Ile Arg Leu Leu Gly Val Cys Ile Glu Met Ser Ser
199                    650                  655                  660
201 caa ggc atc cca aag ccc atg gta att tta ccc ttc atg aaa tac ggg   2131
202 Gln Gly Ile Pro Lys Pro Met Val Ile Leu Pro Phe Met Lys Tyr Gly
203                    665                  670                  675
205 gac ctg cat act tac tta ctt tat tcc cga ttg gag aca gga cca aag   2179
206 Asp Leu His Thr Tyr Leu Leu Tyr Ser Arg Leu Glu Thr Gly Pro Lys
207            680                  685                  690
209 cat att cct ctg cag aca cta ttg aag ttc atg gtg gat att gcc ctg   2227
210 His Ile Pro Leu Gln Thr Leu Leu Lys Phe Met Val Asp Ile Ala Leu
211      695                  700                  705
213 gga atg gag tat ctg agc aac agg aat ttt ctt cat cga gat tta gct   2275
214 Gly Met Glu Tyr Leu Ser Asn Arg Asn Phe Leu His Arg Asp Leu Ala
215 710                    715                  720                  725
217 gct cga aac tgc atc acc cac ctg gcc atc tta gca aga agc cca gca   2323
218 Ala Arg Asn Cys Ile Thr His Leu Ala Ile Leu Ala Arg Ser Pro Ala
219                    730                  735                  740
221 tct tgc tct tac tgc agg ttg cga gat gac atg act gtc tgt gtt gcg   2371
222 Ser Cys Ser Tyr Cys Arg Leu Arg Asp Asp Met Thr Val Cys Val Ala
223            745                  750                  755
225 gac ttc ggc ctc tct aag aag att tac agt ggc gat tat tac cgc caa   2419
226 Asp Phe Gly Leu Ser Lys Lys Ile Tyr Ser Gly Asp Tyr Tyr Arg Gln
227            760                  765                  770
229 ggc cgc att gct aag atg cct gtt aaa tgg atc gcc ata gaa agt ctt   2467
230 Gly Arg Ile Ala Lys Met Pro Val Lys Trp Ile Ala Ile Glu Ser Leu
231      775                  780                  785
233 gca gac cga gtc tac aca agt aaa agt gat gtg tgg gca ttt ggc gtg   2515
234 Ala Asp Arg Val Tyr Thr Ser Lys Ser Asp Val Trp Ala Phe Gly Val
235 790                    795                  800                  805
237 acc atg tgg gaa ata gct acg cgg gga atg act ccc tat cct ggg gtc   2563
238 Thr Met Trp Glu Ile Ala Thr Arg Gly Met Thr Pro Tyr Pro Gly Val
239                    810                  815                  820
241 cag aac cat gag atg tat gac tat ctt ctc cat ggc cac agg ttg aag   2611
242 Gln Asn His Glu Met Tyr Asp Tyr Leu Leu His Gly His Arg Leu Lys
243            825                  830                  835
245 cag ccc gaa gac tgc ctg gat gaa ctg tat gaa ata atg tac tct tgc   2659
246 Gln Pro Glu Asp Cys Leu Asp Glu Leu Tyr Glu Ile Met Tyr Ser Cys
247            840                  845                  850
249 tgg aga acc gat ccc tta gac cgc ccc acc ttt tca gta ttg agg ctg   2707
250 Trp Arg Thr Asp Pro Leu Asp Arg Pro Thr Phe Ser Val Leu Arg Leu
251      855                  860                  865
253 cag cta gaa aaa ctc tta gaa agt ttg cct gac gtt cgg aac caa gca   2755
254 Gln Leu Glu Lys Leu Leu Glu Ser Leu Pro Asp Val Arg Asn Gln Ala
255 870                    875                  880                  885
```

```
257 gac gtt att tac gtc aat aca cag ttg ctg gag agc tct gag ggc ctg    2803
258 Asp Val Ile Tyr Val Asn Thr Gln Leu Leu Glu Ser Ser Glu Gly Leu
259               890             895             900
261 gcc cag ggc tcc acc ctt gct cca ctg gac ttg aac atc gac cct gac    2851
262 Ala Gln Gly Ser Thr Leu Ala Pro Leu Asp Leu Asn Ile Asp Pro Asp
263               905             910             915
265 tct ata att gcc tcc tgc act ccc cgc gct gcc atc agt gtg gtc aca    2899
266 Ser Ile Ile Ala Ser Cys Thr Pro Arg Ala Ala Ile Ser Val Val Thr
267           920             925             930
269 gca gaa gtt cat gac agc aaa cct cat gaa gga cgg tac atc ctg aat    2947
270 Ala Glu Val His Asp Ser Lys Pro His Glu Gly Arg Tyr Ile Leu Asn
271     935             940             945
273 ggg ggc agt gag gaa tgg gaa gat ctg act tct gcc ccc tct gct gca    2995
274 Gly Gly Ser Glu Glu Trp Glu Asp Leu Thr Ser Ala Pro Ser Ala Ala
275 950             955             960             965
277 gtc aca gct gaa aag aac agt gtt tta ccg ggg gag aga ctt gtt agg    3043
278 Val Thr Ala Glu Lys Asn Ser Val Leu Pro Gly Glu Arg Leu Val Arg
279             970             975             980
281 aat ggg gtc tcc tgg tcc cat tcg agc atg ctg ccc ttg gga agc tca    3091
282 Asn Gly Val Ser Trp Ser His Ser Ser Met Leu Pro Leu Gly Ser Ser
283             985             990             995
285 ttg ccc gat gaa ctt ttg ttt gct gac gac tcc tca gaa ggc tca gaa    3139
286 Leu Pro Asp Glu Leu Leu Phe Ala Asp Asp Ser Ser Glu Gly Ser Glu
287         1000            1005            1010
289 gtc ctg atg tga ggagaggtgc ggggagacat tccaaaaatc aagccaattc        3191
290 Val Leu Met  *
291     1015
293 ttctgctgta ggagaatcca attgtacctg atgtttttgg tatttgtctt ccttacc     3248
295 <210> SEQ ID NO: 2
296 <211> LENGTH: 1016
297 <212> TYPE: PRT
298 <213> ORGANISM: Homo sapiens
300 <400> SEQUENCE: 2
301 Met Gly Pro Ala Pro Leu Pro Leu Leu Leu Gly Leu Phe Leu Pro Ala
302 1               5               10              15
303 Leu Trp Arg Arg Ala Ile Thr Glu Ala Arg Glu Glu Ala Lys Pro Tyr
304             20              25              30
305 Pro Leu Phe Pro Gly Pro Phe Pro Gly Ser Leu Gln Thr Asp His Thr
306             35              40              45
307 Pro Leu Leu Ser Leu Pro His Ala Ser Gly Tyr Gln Pro Ala Leu Met
308     50              55              60
309 Phe Ser Pro Thr Gln Pro Gly Arg Pro His Thr Gly Asn Val Ala Ile
310 65              70              75              80
311 Pro Gln Val Thr Ser Val Glu Ser Lys Pro Leu Pro Pro Leu Ala Phe
312             85              90              95
313 Lys His Thr Val Gly His Ile Ile Leu Ser Glu His Lys Gly Val Lys
314             100             105             110
315 Phe Asn Cys Ser Ile Ser Val Pro Asn Ile Tyr Gln Asp Thr Thr Ile
316             115             120             125
```

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 01/10/2005
PATENT APPLICATION: US/10/519,083 TIME: 15:45:01

Input Set : A:\004974.01057 sequence listing.txt.TXT
Output Set: N:\CRF4\01102005\J519083.raw

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:8; N Pos. 640
Seq#:9; N Pos. 266,390,444,480,557,563,569,581,602
Seq#:15; N Pos. 11,577,971

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/519,083

DATE: 01/10/2005
TIME: 15:45:01

Input Set : **A:\004974.01057 sequence listing.txt.TXT**
Output Set: **N:\CRF4\01102005\J519083.raw**

L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:733 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:600
L:752 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:240
M:341 Repeated in SeqNo=9
L:862 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0
M:341 Repeated in SeqNo=15